P2

17. (Amended) The co-complex according to claim 15, wherein said pyridinyl-imidazole inhibitor of p38 is selected from SB203580 or SB202190.

Please add claims 18-22:

18. A method for determining whether a test compound binds to a mutant second serine/threonine protein kinase or a mutant second tyrosine protein kinase, comprising the steps of:

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(a) providing a mutant second serine/threonine or tyrosine protein kinase, wherein said mutant second serine/threonine or tyrosine protein kinase is characterized by:

(i) having at least one close contact amino acid in an ATP binding site changed as compared to an aligned amino acid in an ATP binding site of a corresponding naturally-occurring second serine/threonine or tyrosine protein kinase,

wherein the identity of the changed amino acid corresponds to an aligned close contact amino acid in an ATP binding site of a first serine/threonine or tyrosine protein kinase, and

wherein the second serine/threonine or tyrosine protein kinase is other than said first serine/threonine or tyrosine protein kinase;

(ii) the ability to bind to a compound that is known to bind to an ATP binding site of the first serine/threonine or tyrosine protein kinase, wherein said known compound binds said mutant second serine/threonine or tyrosine protein kinase with a K_i or K_d of less than 10 μM;

(iii) the ability to bind to said known compound with at least a 10-fold lower K_i or K_d than the K_i or K_d for said known compound with said corresponding naturally-occurring second serine/threonine or tyrosine protein kinase;

(b) contacting said test compound with the mutant second serine/threonine or tyrosine protein kinase; and

(c) determining if said test compound binds to said mutant second serine/threonine or tyrosine protein kinase.

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19. The method according to claim 18, wherein said first and said second serine/threonine or tyrosine protein kinases are both MAP kinases.

20. The method according to claim 19, wherein said mutant second serine/threonine or tyrosine protein kinase is selected from:

(a) a mutant ERK2 consisting of the amino acid sequence of SEQ ID NO: 2, wherein amino acid 105 is threonine or alanine; or

(b) a mutant JNK3 comprising amino acids 40-402 of SEQ ID NO: 3, wherein amino acid 146 is threonine or alanine.

21. The method according to claim 20, wherein in SEQ ID NO: 2 amino acid 103 is leucine, amino acid 106 is histidine, amino acid 109 is glycine and amino acid 110 is alanine.

22. The method according to claim 20, wherein in SEQ ID NO: 3 amino acid 150 is glycine.